

FIGURE 1

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGGCTCTCTCTCCCGCAGATCCGAACGGCTGGGCGGGGTCACCCGGGCTGGGA
CAAGAAAGCCCGCGCTGCTGCCCCGGGCCCGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
CGCGCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCCAACCC
GGCACTCAGAGCCCGCAGCGCATCCCGTGCGCCAGCCTCCCGACCCCATCGCCCG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCAGTATGG
ATCCTGGCCGGCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTCTGCGCATCCGTGCCGACGCGCTCGTGGACTGCGCGCGGGGG
CAGAGCGGCACAGTTTGTCTGGAGATCAAGGCAGTCCGTGCGGACCGTGGCCATCAAGGG
CGTGACAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCTCCCGTCTCCCTGAGCAGTGCCAAACAGCGGCAGTGTACAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCCTGCCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCCTGGAGACGACAGCATG
GACCCATTGGGCTTGTACCCGGACTGGAGGCGGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGGCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTTCCATTGGCAGTGCCAGTTTCTAGCTTTAGGAAGAAACATAGAA
TTGTACATATTCAGAGTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCATTCCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACCTCCTTTGGAAAAATCTTATGTCAAGCTGAAATTCCTAATTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAAATTCAGGAACAGGTGATCCACTCTGA
AAACAGCAGGTAAATTTCACTCAACCCATGTGGGAATTGATCTATATCTCTACTTCCAGG
ACCAATTTGCCCTTCCAAATCCCTCCAGGCCAGAAGTGAAGTGGAGCAGGATGGCCCCACAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAAATCCCC
CTGAGGCCAGTTCTGTCACTGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGCACTG
TTCCATCTCCCAGGCCACAGCCCTCTGCCCACCTCACATGCCTCCCATGGATTGGGGCT
CCCAGGCCCCCATGTATGTCAACTGCACTTCTGTGTTCAAAAATCAGGAAAAAGAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCAGCACTTGGTTTTCCACATGATATTTATAGTAAATTTATTTTATGATGTACA
TCTCTTATTTCTTACATTATTTATGCCCCAAATATATTTATGTATGAAGTGGGTTT
TTTTGTATATTAATGGAGTTGTTTGT

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FIGURE 2

MRS GCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLSLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

signal peptide:
amino acids 1-22

N-myristoylation sites:
amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site:
amino acids 48-59

HBGF/FGF domain:
amino acids 80-131

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FIGURE 3A

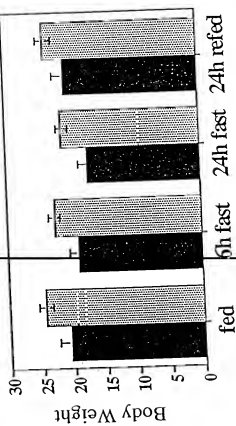


FIGURE 3B

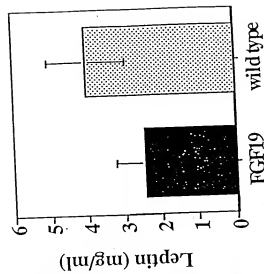


FIGURE 4A

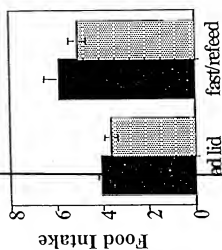


FIGURE 4B

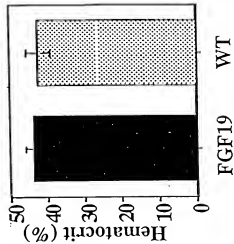
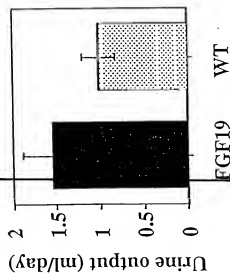
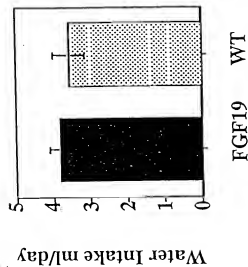


FIGURE 4C

FIGURE 4D

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FIGURE 5

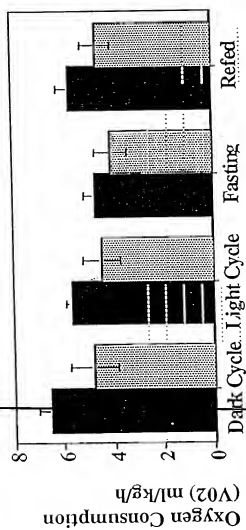


FIGURE 6A

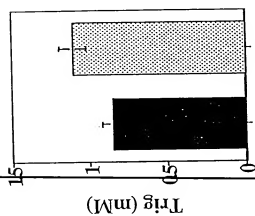


FIGURE 6B

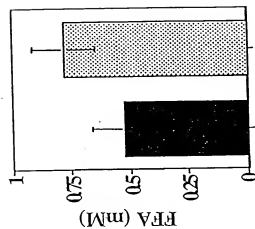


FIGURE 7A

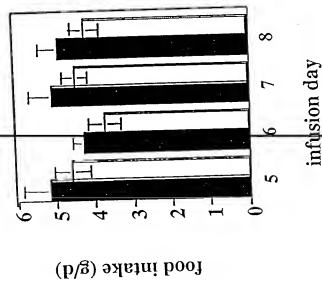
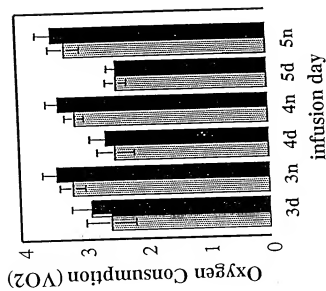


FIGURE 7B



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FIGURE 8A

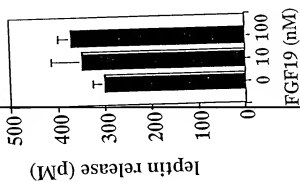
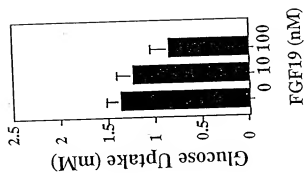


FIGURE 8B



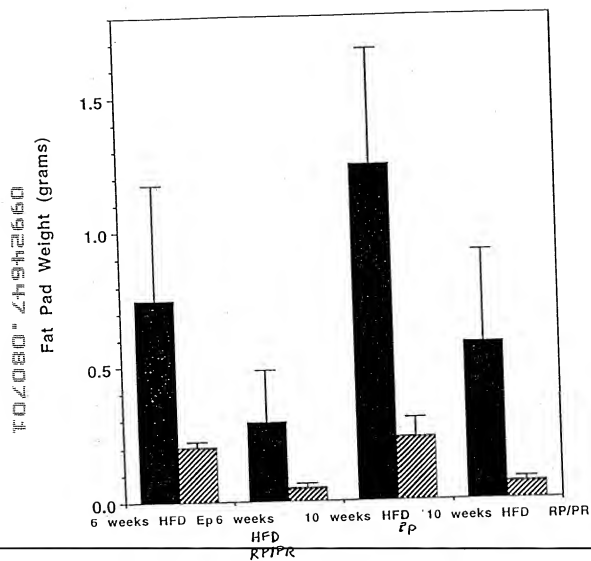


FIGURE 9

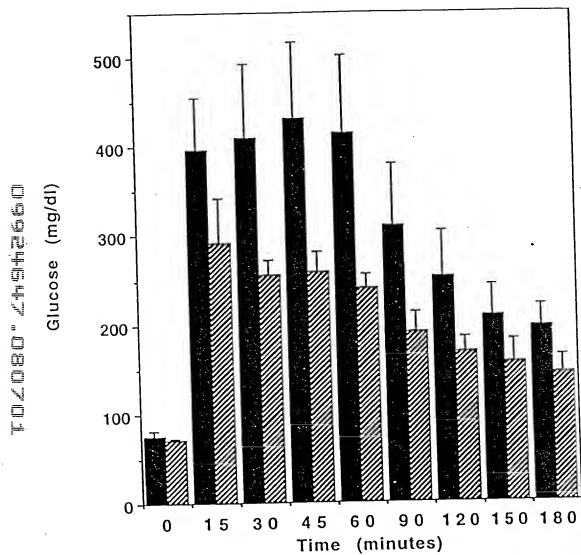
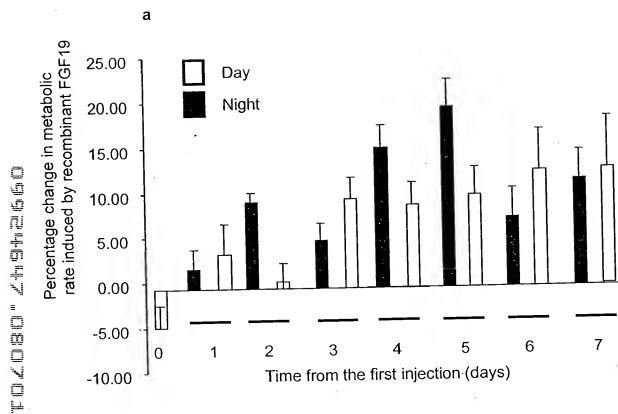


FIGURE 10

Fig. 11



b

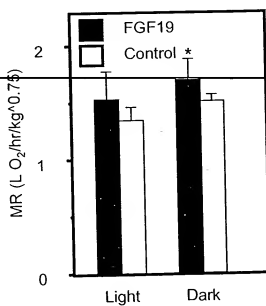


Fig 12

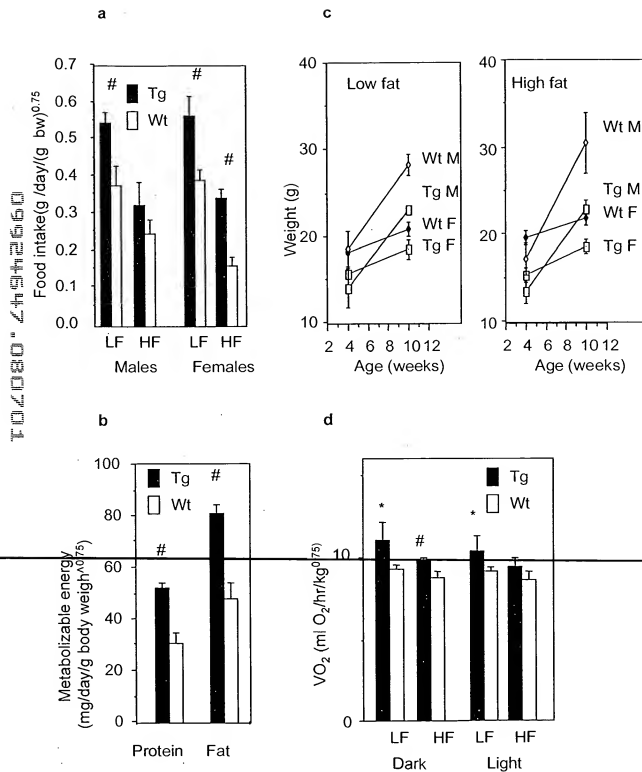


Fig. 13

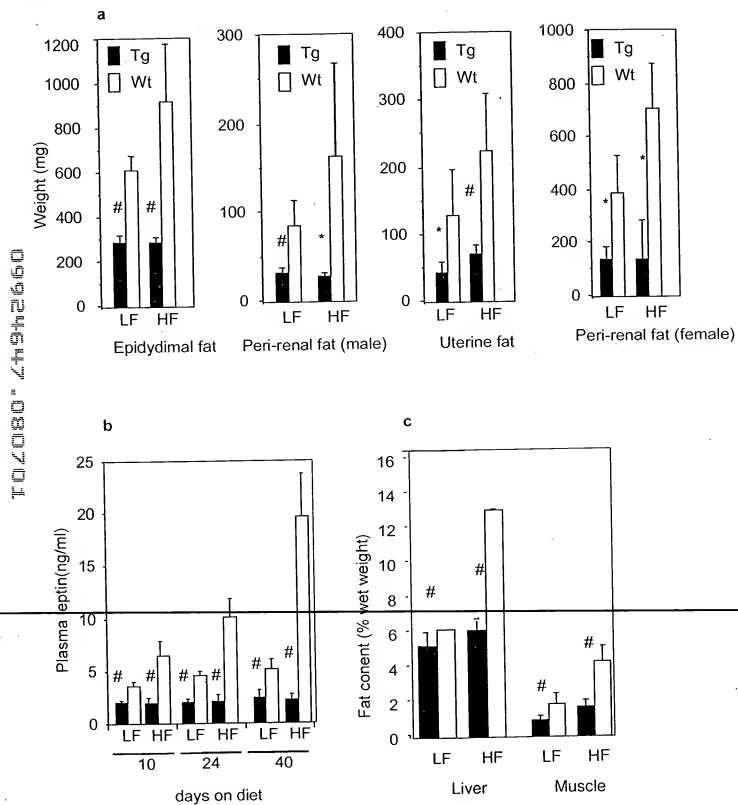


Fig. 14.

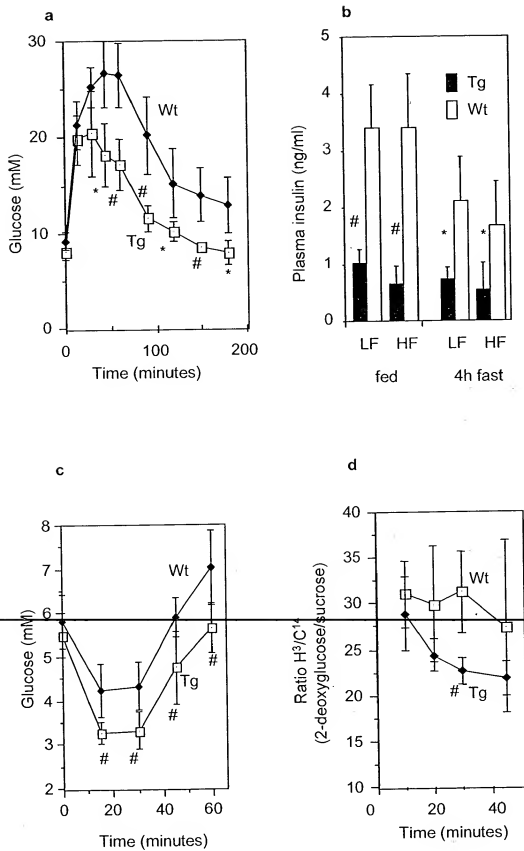


Fig. 15.

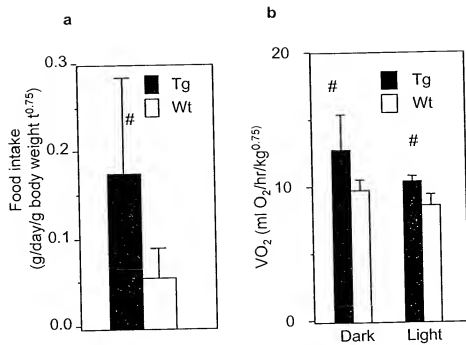
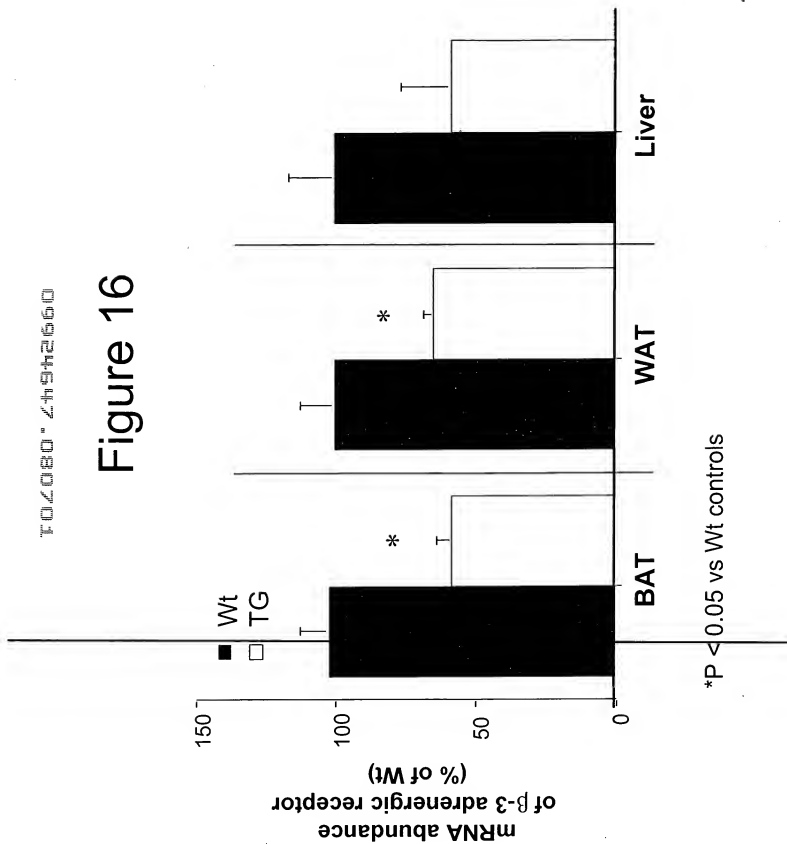
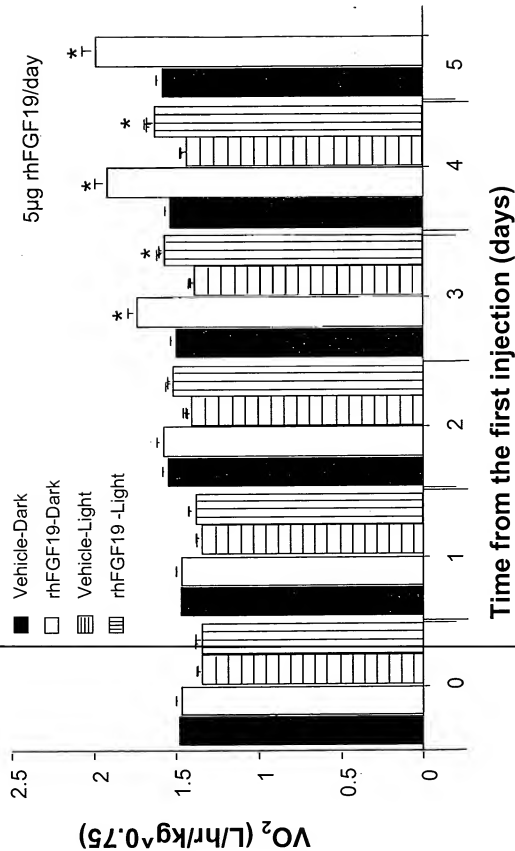


Figure 16



*P < 0.05 vs Wt controls

Figure 17



*P < 0.05 vs Vehicle controls with the same cycle on the same day

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Figure 18

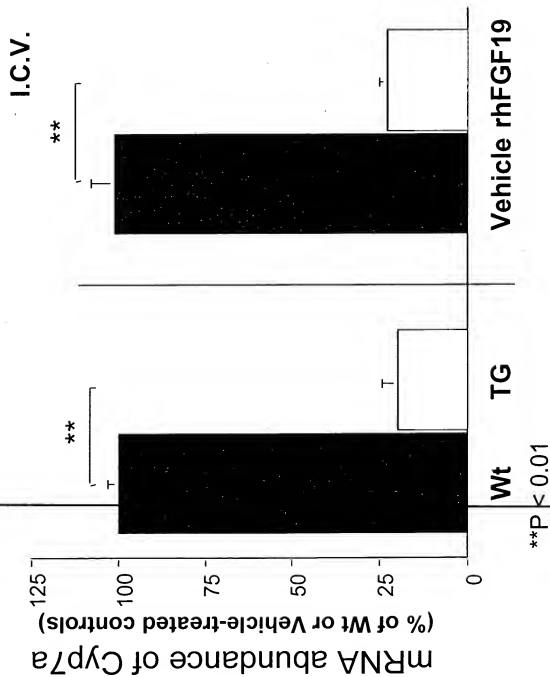


Figure 19

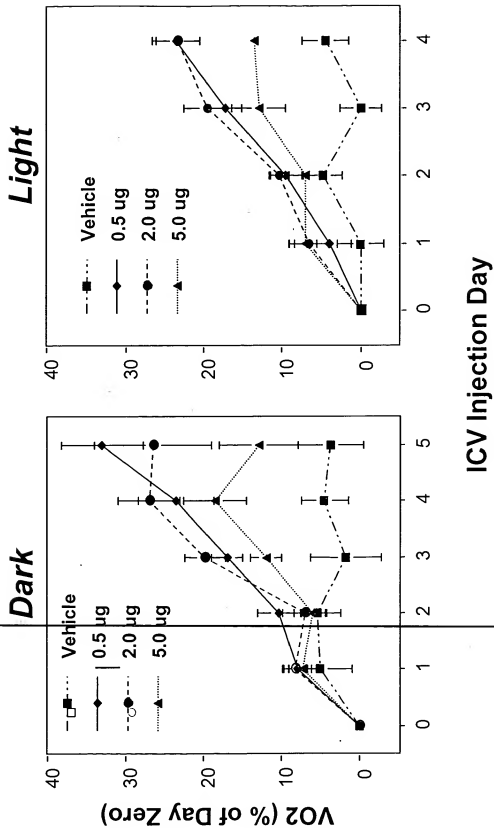


Figure 20

	Vehicle	rhFGF19		
		5.0 μ g	2.0 μ g	0.5 μ g
NPY	1.0 +/- 0.08	0.81 +/- 0.23	0.63 +/- 0.20	0.40 +/- 0.08
AgRP	1.0 +/- 0.33	0.26 +/- 0.10	0.57 +/- 0.26	0.29 +/- 0.16
POMC	1.0 +/- 0.27	1.49 +/- 0.42	3.48 +/- 1.5	38.77 +/- 3.32
MC4-R	1.0 +/- 0.16	0.47 +/- 0.09	0.70 +/- 0.10	0.48 +/- 0.08

